RESULT 1
BTCLAB
bontoxilysin (EC 3.4.24.69) A precursor - Clostridium botulinum
N;Alternate names: botulinum neurotoxin type A
C;Species: Clostridium botulinum
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.
A;Reference number: A35294; MUID:90264400; PMID:2160960
A;Accession: A35294
A;Molecule type: DNA
A;Residues: 1-1296 <BIN>
A;Cross-references: UNIPROT:P10845; UNIPARC:UPI0000001386; GB:M30196; NID:g144864; PIDN:AAA23262.1; PID:g144865
A;Experimental source: strain 62A, subtype A
R;Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.; Melling, J.; Minton, N.P.
Eur. J. Biochem. 189, 73-81, 1990
A;Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding gene.
A;Reference number: S09492; MUID:90235864; PMID:2185020
A;Accession: S09492
A;Molecule type: DNA
A;Residues: 1,'Q',3-26,'V',28-1296 <THO>
A;Cross-references: UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID:g40382
A;Experimental source: NCTC 2916
R;Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins.
A;Reference number: S67988; MUID:96096783; PMID:8521962
A;Accession: S68220
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-12 <FUJ>
A;Cross-references: UNIPARC:UPI0000173655; EMBL:D67030; DDBJ:D50421; NID:g2160224
R;Betley, M.J.; Somers, E.; DasGupta, B.R.
Biochem. Biophys. Res. Commun. 162, 1388-1395, 1989
A;Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-terminal encoding region.
A;Reference number: A33401; MUID:89350959; PMID:2669749
A;Accession: A33401
A;Molecule type: DNA
A;Residues: 1-35 <BET>
A;Cross-references: UNIPARC:UPI000016EA84; GB:M27892; NID:g144880; PIDN:AAA23269.1; PID:g551776
R;Gimenez, J.A.; DasGupta, B.R.
J. Protein Chem. 12, 351-363, 1993
A;Title: Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and 18 kD fragments.
A;Reference number: A53884; MUID:94000342; PMID:8397793
A;Accession: A53884
A;Status: preliminary
A;Molecule type: protein
A;Residues: 867-880;1148-1217,'Y',1219 <GIM>
A;Cross-references: UNIPARC:UPI00000BBB24; UNIPARC:UPI0000173656
A;Experimental source: strain Hall
A;Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after extraction from NCBI backbone

R;DasGupta, B.R.; Dekleva, M.L.
Biochimie 72, 661-664, 1990
A;Title: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site.
A;Reference number: A60025; MUID:91120847; PMID:2126206
A;Accession: A60025
A;Molecule type: protein
A;Residues: 2-6;445-453,'X',455-457 <DAS1>
A;Cross-references: UNIPARC:UPI0000173657; UNIPARC:UPI0000173658
R;DasGupta, B.R.; Foley, J.; Niece, R.
Biochemistry 26, 4162, 1987
A;Title: Partial sequence of the light chain of botulinum neurotoxin type A.
A;Reference number: A27000
A;Accession: A27000
A;Molecule type: protein
A;Residues: 2-47 <DAS2>
A;Cross-references: UNIPARC:UPI0000173659
R;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; Niemann, H.
J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
A;Contents: annotation
C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synapses. This toxin is activated by cleavage into two chains linked by a disulfide bond.
C;Genetics:
A;Gene: atx; botA
C;Function:
A;Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associated 25K protein (SNAP-25)
C;Superfamily: tetanus toxin
C;Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F;2-444/Product: bontoxilysin A light chain #status experimental <LGHT>
F;445-1296/Product: bontoxilysin A heavy chain #status experimental <HVY>
F;223,227/Binding site: zinc (His) #status predicted
F;224/Active site: Glu #status predicted

  Query Match 98.4%; Score 4470.5; DB 1; Length 1296;
  Best Local Similarity 99.3%; Pred. No. 3.6e-218;
  Matches 865; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

```
Qy          1 MEFVNKQFNYKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWVIPERDTFTNPEEGDLN 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPFVNKQFNYKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWVIPERDTFTNPEEGDLN 60

Qy         61 PPPEAKQVPVSYYDSTYLSTDNEKDNYLKGVTKLFERIYSTDLGRMLLTSIVRGIPFWGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PPPEAKQVPVSYYDSTYLSTDNEKDNYLKGVTKLFERIYSTDLGRMLLTSIVRGIPFWGG 120

Qy        121 STIDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STIDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGY 180

Qy        181 GSTQYIRFSPDFTFGFEESLEVDTNPLLGAGKFATDPAVTLAHELIHAGHRLYGIAINPN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSTQYIRFSPDFTFGFEESLEVDTNPLLGAGKFATDPAVTLAHELIHAGHRLYGIAINPN 240

Qy        241 RVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIASTLNKA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIASTLNKA 300
```

```
Qy      301 KSIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLKFDKLYKMLTEIYTEDNFVKFFKV 360
Db      301 KSIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLKFDKLYKMLTEIYTEDNFVKFFKV 360

Qy      361 LNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLRNTNLAANFNGQNTEINNMNFTKLKNFT 420
Db      361 LNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLRNTNLAANFNGQNTEINNMNFTKLKNFT 420

Qy      421 GLFEFYKLLCVRGIITSKTKSLDDDDKGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLNK 480
Db      421 GLFEFYKLLCVRGIITSKTKSL---DKGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLNK 477

Qy      481 GEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIENLSSDIIGQLELMPNIERF 540
Db      478 GEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIENLSSDIIGQLELMPNIERF 537

Qy      541 PNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFSSDYVKKVNKA 600
Db      538 PNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFSSDYVKKVNKA 597

Qy      601 TEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALI 660
Db      598 TEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALI 657

Qy      661 FSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNW 720
Db      658 FSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNW 717

Qy      721 LAKVNTQIDLIRKKMKEALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESI 780
Db      718 LAKVNTQIDLIRKKMKEALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESI 777

Qy      781 NKAMININKFLNQCSVSYLMNSMIPYGVKRLEDFDASLKDALLKYIYDNRGTLIGQVDRL 840
Db      778 NKAMININKFLNQCSVSYLMNSMIPYGVKRLEDFDASLKDALLKYIYDNRGTLIGQVDRL 837

Qy      841 KDKVNNTLSTDIPFQLSKYVDNQRLLSTEEE 871
Db      838 KDKVNNTLSTDIPFQLSKYVDNQRLLSTFTE 868
```